

Evaluation of a type 2 modified live porcine reproductive and respiratory syndrome vaccine against heterologous challenge of a lineage 3 highly virulent isolate in pigs

Fu-Hsiang Hou¹, Wei-Cheng Lee¹, Jiunn-Wang Liao¹, Maw-Sheng Chien¹, Chih-Jung Kuo², Han-Ping Chung², Min-Yuan Chia^{Corresp. 2}

¹ Graduate Institute of Veterinary Pathobiology, National Chung Hsing University, Taichung City, Taiwan (ROC)

² Department of Veterinary Medicine, National Chung Hsing University, Taichung City, Taiwan (ROC)

Corresponding Author: Min-Yuan Chia

Email address: chiaminyuan@dragon.nchu.edu.tw

Porcine reproductive and respiratory syndrome (PRRS) is one of the most common diseases in the global swine industry. PRRSV is characterized by rapid mutation rates and extensive genetic divergences. It is divided into two genotypes, which are composed of several distinct sub-lineages. The purpose of the present study was to evaluate the cross-protective efficacy of Fosterera PRRS MLV, an attenuated lineage 8 strain, against the heterologous challenge of a lineage 3 isolate. Eighteen pigs were randomly divided into mock, MLV and unvaccinated (UnV) groups. The pigs in the MLV group were administered Fosterera PRRS vaccine at 3 weeks of age and both the MLV and UnV groups were inoculated with a virulent PRRSV isolate at 7 weeks. Clinically, the MLV group showed a shorter duration and a lower magnitude of respiratory distress than the UnV group. The average days of fever in the MLV group was 3.0 ± 0.5 , which was significantly lower than the 6.2 ± 0.5 days of the UnV group ($P < 0.001$). The average daily weight gains of the mock, MLV and UnV groups were 781 ± 31 , 550 ± 44 and 405 ± 26 g/day, respectively, during the post-challenge phase. The pathological examinations revealed that the severity of interstitial pneumonia in the MLV group was milder compared to the UnV group.

Furthermore, PRRSV viremia titers in the MLV pigs were consistently lower (10^1 - $10^{1.5}$ genomic copies) than those of the UnV pigs from 4 to 14 DPC. In conclusion, vaccination with Fosterera PRRS MLV confers partial cross-protection against heterologous challenge of a virulent lineage 3 PRRSV isolate.

1

2 **Evaluation of a type 2 modified live porcine reproductive**
3 **and respiratory syndrome vaccine against heterologous**
4 **challenge of a lineage 3 highly virulent isolate in pigs**

5

6

7 Fu-Hsiang Hou¹, Wei-Cheng Lee¹, Jiunn-Wang Liao¹, Maw-Sheng Chien¹, Chih-Jung Kuo²,
8 Han-Ping Chung², Min-Yuan Chia²

9

10 ¹ Graduate Institute of Veterinary Pathobiology, National Chung Hsing University, Taichung
11 City, Taiwan (R.O.C.)

12 ² Department of Veterinary Medicine, National Chung Hsing University, Taichung City, Taiwan
13 (R.O.C.)

14

15 Corresponding Author:

16 Min-Yuan Chia²

17 145 Xingda Rd., South Dist., Taichung City, 402, Taiwan (R.O.C.)

18 Email address: chiaminyuan@dragon.nchu.edu.tw

19

20 Abstract

21 Porcine reproductive and respiratory syndrome (PRRS) is one of the most common diseases
22 in the global swine industry. PRRSV is characterized by rapid mutation rates and extensive
23 genetic divergences. It is divided into two genotypes, which are composed of several distinct
24 sub-lineages. The purpose of the present study was to evaluate the cross-protective efficacy of
25 Fostera PRRS MLV, an attenuated lineage 8 strain, against the heterologous challenge of a
26 lineage 3 isolate. Eighteen pigs were randomly divided into mock, MLV and unvaccinated
27 (UnV) groups. The pigs in the MLV group were administered Fostera PRRS vaccine at 3 weeks
28 of age and both the MLV and UnV groups were inoculated with a virulent PRRSV isolate at 7
29 weeks. Clinically, the MLV group showed a shorter duration and a lower magnitude of
30 respiratory distress than the UnV group. The average days of fever in the MLV group was
31 3.0 ± 0.5 , which was significantly lower than the 6.2 ± 0.5 days of the UnV group ($P<0.001$). The
32 average daily weight gains of the mock, MLV and UnV groups were 781 ± 31 , 550 ± 44 and
33 405 ± 26 g/day, respectively, during the post-challenge phase. The pathological examinations
34 revealed that the severity of interstitial pneumonia in the MLV group was milder compared to
35 the UnV group. Furthermore, PRRSV viremia titers in the MLV pigs were consistently lower
36 (10^1 - $10^{1.5}$ genomic copies) than those of the UnV pigs from 4 to 14 DPC. In conclusion,
37 vaccination with Fostera PRRS MLV confers partial cross-protection against heterologous
38 challenge of a virulent lineage 3 PRRSV isolate.

39

40 Introduction

41 Porcine reproductive and respiratory syndrome (PRRS) is one of the most common and
42 economically important diseases in the global swine industry. PRRSV causes respiratory distress
43 in nursery pigs and late-term abortion in breeding herds. The etiologic agent, PRRSV, is a
44 spherical, enveloped, single-strand, positive-sense RNA virus with sizes ranging from about 45-
45 70 nm in diameter, and is characterized by rapid mutation rates and extensive genetic divergence
46 (Cho & Dee 2006). PRRSV was originally divided into genotype I (European) and genotype II
47 (North American), which have been recently reclassified into the *Betaarterivirus* genus,
48 *Arteriviridae* family as two species: *Betaarterivirus suis 1* and *Betaarterivirus suis 2* (Stoian &
49 Rowland 2019). The genetic variation between these two types is approximately 40% at the
50 nucleotide level (Nelsen et al. 1999). The type II viruses are further sub-classified into nine
51 distinct lineages based on sequences of open reading frame 5 (ORF5) (Shi et al. 2010). In
52 Taiwan, PRRSVs predominantly belong to lineage 3 of type II and are circulating in almost all
53 pig farms (Deng et al. 2015). In our previous study, some highly virulent lineage 3 strains were
54 able to trigger considerable economical losses (30% mortality in the nursery phase) in the field
55 and could induce severe clinical signs and high mortality in healthy experimental pigs (Hou et al.
56 2019). In addition, lineage 3 PRRSV has also been recognized sporadically in the South-East
57 China and Hong Kong regions since 2010 (Shi et al. 2010). Currently, one recombinant lineage 3
58 PRRSV was reported to have re-emerge with increased pathogenicity, and later became one of
59 the most prevalent PRRSV clusters in China in 2018 (Guo et al. 2018; Lu et al. 2015).

60 For controlling PRRS, vaccination is an important strategy and has been broadly implemented
61 in many countries. However, due to the broad divergence and great heterogeneity in terms of
62 antigenicity and pathogenicity, the reliability of global universal vaccines to confront divergent
63 PRRSV field strains, particularly in different types or lineages, has remained questionable for
64 decades (Li et al. 2014; Lunney et al. 2016). Recently, a commercial PRRS modified-live virus
65 (MLV) vaccine, Fosterera PRRS (Zoetis), has become available in Taiwan. This MLV vaccine was
66 derived from a US PRRSV isolate (P129) that was sequentially attenuated in a porcine-
67 originated cell line, rather than other species. To the best of our knowledge, it has been proven
68 that Fosterera PRRS can elicit immunogenicity and broad cross-protection against lineages 1, 5, 8
69 and 9 of type II and even type I PRRSV (Calvert et al. 2017; Choi et al. 2016; Do et al. 2015;
70 Park et al. 2015; Park et al. 2014; Savard et al. 2016). However, there is very little information
71 regarding the cross-protection of commercial vaccines against lineage 3 of type II PRRSV so far.
72 The purpose of the present study was to evaluate the cross-protective efficacy of Fosterera PRRS
73 MLV against heterologous challenge of a virulent lineage 3 PRRSV field isolate.

74

75 **Materials & Methods**

76 **Virus and Cells**

77 The PRRSV field strain (TSYM-142575; GenBank: KY769953) used in the present study was
78 originally isolated from a farm in Taiwan with severe post-weaning respiratory distress and
79 continuously high mortalities between 2014 and 2017 (Hou et al. 2019). Briefly, tissue samples
80 from TSYM-infected pigs were homogenized, centrifuged, filtered and inoculated. The inocula
81 was prepared by four-passage inoculation on pulmonary alveolar macrophages (PAM) for use in
82 pig challenges and 10 further propagations on a MARC-145 cell line (ATCC CRL-12231) for
83 neutralizing antibody and ELISpot assays in this study. The viral stocks were tittered for
84 calculating the 50% tissue culture infective dose (TCID₅₀) and identified by reverse transcription
85 polymerase chain reaction (RT-PCR) and gene sequencing. The TSYM-isolate was classified
86 into lineage 3 of type II PRRSV by phylogenetic analysis and shared 85.7% ORF5 identity at the
87 nucleotide level with the P129 vaccine strain (GenBank: AF494042). Meanwhile, both stocks
88 were confirmed negative for pseudorabies virus (PRV), type II porcine circovirus (PCV2) and
89 classical swine fever virus (CSFV) by molecular assays.

90

91 **Animal experiment**

92 Eighteen male, Landrace-Yorkshire pigs were introduced from a PRRSV, PRV, and CSFV-
93 free pig farm at the age of 18 days. All pigs were negative for PRRSV under ELISA and real-
94 time RT-PCR detections. The pigs were randomly divided into three groups (six pigs for each
95 group) by using the Random function (EXCEL, Microsoft) and raised in separate rooms. The
96 MLV pigs were administered Fosterera PRRS MLV vaccines (LOT: 251726A; Zoetis) at 3 weeks
97 of age (-28 day-post challenge; -28 DPC). Pigs in the unvaccinated (UnV) and mock control
98 groups received saline as a placebo on the same day. Four weeks after the vaccination (0 DPC),
99 the MLV and UnV groups were intra-nasally and intra-muscularly inoculated with 10⁶ TCID₅₀ of

100 TSYM-strain PRRSV inocula. The mock pigs were administered a PAM culture medium instead.
101 Blood samples were taken at -28, -21, -14, -7, 0, 4, 7, 10, 14 and 21 DPC for serological and
102 virological analysis. During the experimental period, all clinical and laboratory personnel were
103 blind to swine groups and samples. All pigs were then humanely euthanized by electrical
104 stunning and exsanguination for pathological examination at 21 DPC. The experiment was
105 conducted within the experimental house of the Graduate Institute of Veterinary Pathobiology
106 according to animal ethical principles and the protocol was approved by the Institutional Animal
107 Care and Use Committee of National Chung Hsing University (IACUC number: 107-045).

108

109 **Clinical observations**

110 Clinical signs were evaluated at the same time every morning by the same investigator. The
111 body temperatures were simultaneously detected by using BioThermo LifeChips implants
112 (Destron Fearing) and classified as fever when temperatures were above 40 °C. Clinical scores
113 were evaluated for activity, ranging from 0 (normal) to 3 (severe), and respiratory distress,
114 ranging from 0 (normal) to 6 (severe), following the guidelines of previous studies (Halbur et al.
115 1995; Jolie et al. 1995). Individual body weights were measured at -28, 0, 10 and 21 DPC for
116 average daily weight gain (ADWG) calculations. The amounts of daily food intake (FI) and the
117 food conversion rate (FCR) were also recorded for measuring the appetite and growth
118 performance of the pigs.

119

120 **Viremia and serological measurement**

121 Serum samples were submitted for real-time RT-PCR for PRRSV quantification as previously
122 described (Hou et al. 2019). The PRRSV-specific antibody was measured by using IDEXX
123 PRRSX3 Ab test kits and strictly following the manufacturer's instructions. The serum
124 neutralizing antibody assay was performed according to previous methods (Chia et al. 2010;
125 Yoon et al. 1994).

126

127 **Pathological evaluation**

128 The severities of both macro- and microscopic lung lesions were scored as previously
129 described by three pathologists under blind tests (Halbur et al. 1995).

130

131 **PRRSV-specific IFN- γ ELISpot assay**

132 PRRSV-specific interferon-gamma (IFN- γ) responses were measured by using pre-coated
133 porcine IFN- γ ELISpot plates (Mabtech) according to the manufacturer's directions and previous
134 studies (Park et al. 2014).

135

136 **Statistical analysis**

137 All statistical analysis was performed using IBM SPSS statistical software (version 20).
138 Continuous data, including fever day, ADWG, viremia and serology, were verified for the
139 normality (Shapira-Wilk test) and homogeneity of variance (Levene test) and measured for

140 statistical significance by using ANOVA and Student's *t* test. Post Hoc analysis was then done
141 by Tukey's test. For not normally distributed and categorical data, including body temperature,
142 clinical scores, lung lesion scores and ELISpot, Kruskal-Wallis and Mann-Whitney tests were
143 rather applied. Statistical significances were defined as a *P* value less than 0.05.

144

145 **Results**

146 **Animal exclusion and mortality**

147 During the experimental period, one pig from the MLV group was excluded due to PRRSV-
148 unrelated death. The pig showed acute clinical signs (including open-mouth breathing, vomiting,
149 and cyanosis) after 5 minutes of administration with viral inoculum and died immediately.
150 Pathological examination showed massive edema and hemorrhage in multiple viscera. These
151 findings indicated that a severe anaphylactic reaction was induced by viral inoculum and the
152 death was not caused by PRRSV infection.

153 One pig from the UnV group was humanely euthanized at 14 DPC due to severe depression,
154 anorexia and dyspnea. Proliferative necrotizing pneumonia and non-suppurative encephalitis
155 were noted during histopathological examination, which were frequently observed after
156 challenge with virulent TSYM-isolate in our previous study (Hou et al. 2019). The PRRSV
157 viremia titer reached 7.14 copies/ μ L and showed no decline until death.

158 As stated above, the final PRRSV-associated mortality rates of the mock, MLV and UnV
159 groups were 0, 0 and 17%, respectively, in the present study.

160

161 **Changes in body temperature**

162 Following TSYM-strain challenge, the UnV group presented persistent fever (≥ 40 °C) from 1
163 to 13 DPC. The MLV group showed slightly raised body temperatures after challenge and then
164 gradually recovered from 4 DPC (Fig. 1A). Briefly, the level of fever in the MLV group was
165 milder than that in the UnV group, and the average days of fever in the MLV group (3.0 ± 0.5)
166 was also significantly lower than the UnV group (6.2 ± 0.5) ($P < 0.001$; Fig. 1B). The temperature
167 values of the mock group remained steady during the challenge period.

168

169 **Clinical signs and growth performance**

170 After challenge, the UnV group showed high morbidity in terms of significant depression
171 during 5-13 DPC, and signs of respiratory distress gradually developed from 8 DPC, with
172 notable distress persisting until the end of the trial. In contrast, most of the pigs in the MLV
173 group showed only mild depression after challenge, and the magnitude of respiratory distress
174 was consistently less than the UnV group throughout this experiment (Fig. 2).

175 Prior to challenge, the average body weights were 16.6 ± 0.3 , 17.8 ± 0.4 , 17.4 ± 0.1 kg for the
176 mock, UnV and MLV groups, respectively, and no statistically significant differences were
177 apparent among these three groups. However, the ADWG of the UnV group was significantly
178 decreased compared to that of the MLV and mock groups in both the acute and whole infection
179 periods, as shown in Fig. 3. The average productivity of the UnV group was only 13% (98 g/day)

180 of the mock group (763 g/day) in the acute phase. In contrast, a lesser degree of growth
181 retardation was observed in the MLV group, with 80% preservation of the ADWG compared to
182 the mock pigs. Similarly, the amounts of food intake and the food conversion ratio also revealed
183 the same trends among the different groups.

184

185 **Macroscopic and microscopic lung lesion scores**

186 As shown in Fig. 4A, the mean macroscopic lesion areas of the UnV and MLV groups were
187 37.8 ± 11.3 and $19.6 \pm 6.1\%$. The UnV group showed significantly more severe interstitial
188 pneumonia ($P < 0.01$) than those in the mock group, and the MLV group showed milder
189 interstitial pneumonia compared to the UnV group ($P = 0.12$). Histopathologically, the mean
190 microscopic scores were 1.97 ± 0.19 and 1.36 ± 0.09 for the UnV and MLV groups, respectively
191 (Fig. 4B and Fig. S1). The differences in severity of microscopic interstitial pneumonia were
192 significant between the UnV and mock group ($P < 0.01$), but not reach a significant level between
193 the MLV and mock groups ($P = 0.16$). Both the macro- and microscopic lesion scores of the mock
194 pigs showed no evidence of PRRSV-associated lung lesions.

195

196 **PRRSV viremia quantification**

197 Following vaccination, low viremia titers in the MLV group were detected at -14 DPC (14
198 days post-vaccination; 14 DPV; viral titer $1.87 \pm 0.27 \log_{10}$ copies/ μL) and 0 DPC (28 DPV; viral
199 titer $0.87 \pm 0.26 \log_{10}$ copies/ μL), and the UnV and mock groups remained undetectable before
200 challenge (Fig. 5). After challenge with the TSYM-strain, viremia was detected as early as 4
201 DPC in all challenge groups. At 4 DPC, the UnV pigs displayed high serum viral titers
202 ($6.84 \pm 0.23 \log_{10}$ copies/ μL) and were significantly higher ($P < 0.05$) than that of the MLV group.
203 Meanwhile, the serum viral titer of the MLV group was 10^1 to $10^{1.5}$ less than that of the UnV
204 group at 7, 10 and 14 DPC ($P = 0.18, 0.08$ and 0.22 , respectively). PRRSV nucleic acid was not
205 detected in the serum of the mock pigs throughout this study.

206

207 **Serological response**

208 As shown in Fig. 6A, all pigs were negative for PRRSV-specific IgG antibodies at the time of
209 vaccination (0 DPV; -28 DPI) and seroconversion was first detected at 14 DPV in the MLV
210 group. All vaccinated pigs were seropositive for PRRSV-specific antibodies at 0 DPC and the
211 MLV group had significantly higher ($P < 0.05$) antibody titers than those of the UnV group at 7
212 DPC. The mock group showed no PRRSV-specific IgG antibodies throughout this trial.
213 In the neutralizing antibody assay, no groups showed neutralizing effects in response to the
214 challenge strain (less than 2).

215

216 **Responses of PRRSV-specific IFN- γ secreting cells**

217 The cellular response was evaluated in frequencies of IFN- γ SC in PBMC. Prior to challenge
218 (0 DPC), the frequencies of PRRSV-specific IFN- γ SC in all groups were less than an average of
219 10 cells per 10^6 PBMC. Upon challenge with the TSYM-strain, the frequency of PRRSV-

220 specific IFN- γ SC reached an average of 13.8 ± 8.9 and 26.0 ± 9.5 cells per 10^6 PBMC at 21 DPC
221 in the UnV and MLV groups, respectively (Fig. 6B). The result of Kruskal-Wallis test indicated
222 that the P value was 0.08, and Post Hoc analysis revealed a moderate difference between the
223 mock and MLV group at the time of 21 DPC ($P=0.07$).

224

225 Discussion

226 Vaccination is one of the most common strategies for controlling PRRS. However, the
227 efficacy depends largely on the immunogenicity of the vaccine strain itself and the antigenic
228 similarity with divergent PRRS isolates. In the current study, the commercial vaccine strain,
229 Fosterera PRRS, belonged to lineage 8 of type II PRRSV and shared only 85.7% nucleic acid
230 identity of the ORF5 sequence with the lineage 3 challenge PRRSV, TSYM-strain. This genetic
231 difference clearly indicated the heterology between these two strains (Shi et al. 2010). However,
232 the Fosterera PRRS MLV vaccine still showed partial cross-protective efficacy against a
233 heterologous and virulent PRRSV field strain after challenge in this experiment.

234 For the particular purpose of evaluating the protection of vaccination against rigorous PRRSV
235 infection, this trial consisted of challenge with a highly virulent PRRSV strain by simultaneous
236 intranasal and intramuscular administration. In our previous experience, this challenge model
237 could trigger obvious respiratory disorders, growth retardation, prolonged pyrexia and 20 to 40%
238 mortality in healthy 8-week-old pigs, which was similar to the results produced in the UnV group
239 in this study. In contrast, pigs immunized with Fosterera PRRS vaccine experienced fevers that
240 were shorter in duration and lower in magnitude, improvement of activity, and lowered
241 respiratory distress. Appetites were also improved in the vaccinated group, especially within the
242 acute phase of PRRSV infection. These improvements were further reflected in the significant
243 advance in growth performance in the vaccinated group. Furthermore, pigs vaccinated with
244 Fosterera PRRS vaccine showed an obvious decrease in the severity of interstitial pneumonia,
245 compared to the UnV group, in terms of both macro- and microscopic evaluations, which might
246 sequentially contribute to the maintenance of the feed conversion rate after challenge.

247 PRRSV viremic titers are also one of the most important parameters and are strongly
248 correlated with the outcomes of PRRSV infection (Labarque et al. 2003). In this challenge
249 model, the virulent TSYM-strain triggered high viremia titers ($6.84\pm 0.23 \log_{10}$ copies/ μ L) of
250 PRRSV in the UnV pigs and this level of viral titer was similar to those of highly pathogenic-
251 PRRSV (Guo et al. 2013; Park et al. 2015). In this study, the mean values of PRRSV viremic
252 titer of the MLV group was consistently lower than that of the UnV group during the period from
253 4 to 21 DPC. And it is also worth noting that the vaccine-induced protection occurred very early
254 in this study, which was in accordance with the clinical observations and growth performance.

255 The adaptive immune responses to PRRSV have generally been described as weak, which
256 results in delayed elimination of the virus from the host. This predicament could even occur in
257 vaccinated pigs and is worse when heterogeneity exists between the vaccine and the exposed
258 strains (Costers et al. 2009; Li et al. 2014). In the present study, although the robust PRRSV-
259 specific IgG antibodies were detected from 14 DPV in the MLV group, none of the neutralizing

260 antibody was detected within 3 weeks after challenge. In the several previous studies, even
261 though MLV could not induce neutralizing antibodies in the sera, MLV could confer cross-
262 protection against heterologous challenge (Do et al. 2015; Li et al. 2014; Park et al. 2015). Our
263 results were similar to previous studies involving challenge with heterologous PRRSV in
264 vaccinated pigs, and logistically revealed that humoral immunity was not a major contributor to
265 the early protection. For cell-mediated immunity, IFN- γ is known to inhibit the replication of
266 PRRSV in macrophages and is associated with cytotoxic immunity activation (Bautista &
267 Molitor 1999; Loving et al. 2015; Lunney et al. 2016). Although variations existed in the IFN- γ -
268 SC measurement, vaccine group still showed a higher recalling response while stimulated with
269 the challenge virus compared to the UnV group (Ferrari et al. 2013; Kim et al. 2015). However,
270 despite the importance of conventional pathway in adaptive immunities, other immunological
271 mechanisms had also been claimed in many previous literatures, such as IL-10 cytokine
272 modulation, and could be established by MLV vaccination and sequentially alleviated the
273 impairments of PRRSV infection (Do et al. 2015; Lunney et al. 2016; Park et al. 2015; Park et al.
274 2014).

275 It has been reported in previous studies that vaccination with commercial attenuated PRRSV
276 vaccine might have adverse effects on growth performance, and subsequent shedding of the
277 vaccine virus allows spread from pigs to the environment (Opriessnig et al. 2005; Park et al.
278 2015; Savard et al. 2016). Although the Fosterera PRRS vaccination did elicit a low titer of
279 PRRSV viremia for at least 4 weeks, neither clinical signs nor notable body temperature changes
280 were observed throughout the period after vaccination (data not shown). Also, body weight
281 losses were not observed in this trial.

282

283 **Conclusions**

284 To the best of our knowledge, this is the first evaluation of commercial Fosterera PRRS vaccine
285 (lineage 8) against challenge with a highly virulent field strain (lineage 3). The present study
286 demonstrates that vaccination with Fosterera PRRS MLV confers partial cross-protection against
287 heterologous challenge of a virulent lineage 3 PRRSV isolate.

288

289 **Acknowledgements**

290 The authors would like to thank Ian Cochrane-Lusk for English revision of the manuscript.

291

292 **References**

- 293 Bautista EM, and Molitor TW. 1999. IFN gamma inhibits porcine reproductive and respiratory
294 syndrome virus replication in macrophages. *Archives of Virology* 144:1191-1200.
- 295 Calvert JG, Keith ML, Pearce DS, Lenz MC, King VL, Diamondidis YA, Ankenbauer RG, and
296 Martinon NC. 2017. Vaccination against porcine reproductive and respiratory syndrome
297 virus (PRRSV) reduces the magnitude and duration of viremia following challenge with a
298 virulent heterologous field strain. *Veterinary Microbiology* 205:80-83. DOI:
299 10.1016/j.vetmic.2017.03.037

- 300 Chia MY, Hsiao SH, Chan HT, Do YY, Huang PL, Chang HW, Tsai YC, Lin CM, Pang VF, and
301 Jeng CR. 2010. The immunogenicity of DNA constructs co-expressing GP5 and M
302 proteins of porcine reproductive and respiratory syndrome virus conjugated by GPGP
303 linker in pigs. *Veterinary Microbiology* 146:189-199. DOI: 10.1016/j.vetmic.2010.05.007
- 304 Cho JG, and Dee SA. 2006. Porcine reproductive and respiratory syndrome virus.
305 *Theriogenology* 66:655-662. DOI: 10.1016/j.theriogenology.2006.04.024
- 306 Choi K, Park C, Jeong J, Kang I, Park SJ, and Chae C. 2016. Comparison of commercial type 1
307 and type 2 PRRSV vaccines against heterologous dual challenge. *Veterinary Record*
308 178:291. DOI: 10.1136/vr.103529
- 309 Costers S, Lefebvre DJ, Goddeeris B, Delputte PL, and Nauwynck HJ. 2009. Functional
310 impairment of PRRSV-specific peripheral CD3⁺CD8^{high} cells. *Veterinary Research*
311 40:46. DOI: 10.1051/vetres/2009029
- 312 Deng MC, Chang CY, Huang TS, Tsai HJ, Chang C, Wang FI, and Huang YL. 2015. Molecular
313 epidemiology of porcine reproductive and respiratory syndrome viruses isolated from
314 1991 to 2013 in Taiwan. *Archives of Virology* 160:2709-2718. DOI: 10.1007/s00705-
315 015-2554-4
- 316 Do DT, Park C, Choi K, Jeong J, Nguyen TT, Nguyen KD, Vo DT, and Chae C. 2015.
317 Comparison of two genetically distant type 2 porcine reproductive and respiratory
318 syndrome virus (PRRSV) modified live vaccines against Vietnamese highly pathogenic
319 PRRSV. *Veterinary Microbiology* 179:233-241. DOI: 10.1016/j.vetmic.2015.06.013
- 320 Ferrari L, Martelli P, Saleri R, De Angelis E, Cavalli V, Bresaola M, Benetti M, and Borghetti P.
321 2013. Lymphocyte activation as cytokine gene expression and secretion is related to the
322 porcine reproductive and respiratory syndrome virus (PRRSV) isolate after in vitro
323 homologous and heterologous recall of peripheral blood mononuclear cells (PBMC) from
324 pigs vaccinated and exposed to natural infection. *Veterinary Immunology and*
325 *Immunopathology* 151:193-206. DOI: 10.1016/j.vetimm.2012.11.006
- 326 Guo B, Lager KM, Henningson JN, Miller LC, Schlink SN, Kappes MA, Kehrli ME, Jr.,
327 Brockmeier SL, Nicholson TL, Yang HC, and Faaberg KS. 2013. Experimental infection
328 of United States swine with a Chinese highly pathogenic strain of porcine reproductive
329 and respiratory syndrome virus. *Virology* 435:372-384. DOI: 10.1016/j.virol.2012.09.013
- 330 Guo Z, Chen XX, Li R, Qiao S, and Zhang G. 2018. The prevalent status and genetic diversity of
331 porcine reproductive and respiratory syndrome virus in China: a molecular
332 epidemiological perspective. *Virology Journal* 15:2. DOI: 10.1186/s12985-017-0910-6
- 333 Halbur PG, Paul PS, Frey ML, Landgraf J, Eernisse K, Meng XJ, Lum MA, Andrews JJ, and
334 Rathje JA. 1995. Comparison of the pathogenicity of two US porcine reproductive and
335 respiratory syndrome virus isolates with that of the Lelystad virus. *Veterinary Pathology*
336 32:648-660. DOI: 10.1177/030098589503200606
- 337 Hou FH, Chia MY, Lee YH, Liao JW, and Lee WC. 2019. A comparably high virulence strain of
338 porcine reproductive and respiratory syndrome virus isolated in Taiwan. *Comparative*
339 *Immunology, Microbiology and Infectious Diseases* 65:96-102. DOI:
340 10.1016/j.cimid.2019.05.008
- 341 Jolie RA, Mulks MH, and Thacker BJ. 1995. Cross-protection experiments in pigs vaccinated
342 with *Actinobacillus pleuropneumoniae* subtypes 1A and 1B. *Veterinary Microbiology*
343 45:383-391. DOI: 10.1016/0378-1135(94)00145-M
- 344 Kim T, Park C, Choi K, Jeong J, Kang I, Park SJ, and Chae C. 2015. Comparison of two
345 commercial type 1 porcine reproductive and respiratory syndrome virus (PRRSV)

- 346 modified live vaccines against heterologous type 1 and type 2 PRRSV challenge in
347 growing pigs. *Clinical and Vaccine Immunology*. DOI: 10.1128/CVI.00001-15
- 348 Labarque G, Van Gucht S, Van Reeth K, Nauwynck H, and Pensaert M. 2003. Respiratory tract
349 protection upon challenge of pigs vaccinated with attenuated porcine reproductive and
350 respiratory syndrome virus vaccines. *Veterinary Microbiology* 95:187-197.
- 351 Li X, Galliher-Beckley A, Pappan L, Tribble B, Kerrigan M, Beck A, Hesse R, Blecha F, Nietfeld
352 JC, Rowland RR, and Shi J. 2014. Comparison of host immune responses to homologous
353 and heterologous type II porcine reproductive and respiratory syndrome virus (PRRSV)
354 challenge in vaccinated and unvaccinated pigs. *Biomed Res Int* 2014:416727. DOI:
355 10.1155/2014/416727
- 356 Loving CL, Osorio FA, Murtaugh MP, and Zuckermann FA. 2015. Innate and adaptive
357 immunity against porcine reproductive and respiratory syndrome virus. *Veterinary
358 Immunology and Immunopathology* 167:1-14. DOI: 10.1016/j.vetimm.2015.07.003
- 359 Lu WH, Tun HM, Sun BL, Mo J, Zhou QF, Deng YX, Xie QM, Bi YZ, Leung FC, and Ma JY.
360 2015. Re-emerging of porcine respiratory and reproductive syndrome virus (lineage 3)
361 and increased pathogenicity after genomic recombination with vaccine variant.
362 *Veterinary Microbiology* 175:332-340. DOI: 10.1016/j.vetmic.2014.11.016
- 363 Lunney JK, Fang Y, Ladinig A, Chen N, Li Y, Rowland B, and Renukaradhya GJ. 2016. Porcine
364 reproductive and respiratory syndrome virus (PRRSV): pathogenesis and interaction with
365 the immune system. *Annual Review of Animal Biosciences* 4:129-154. DOI:
366 10.1146/annurev-animal-022114-111025
- 367 Nelsen CJ, Murtaugh MP, and Faaberg KS. 1999. Porcine reproductive and respiratory syndrome
368 virus comparison: divergent evolution on two continents. *Journal of Virology* 73:270-
369 280.
- 370 Opriessnig T, Pallares FJ, Nilubol D, Vincent AL, Thacker EL, Vaughn EM, Roof M, and
371 Halbur PG. 2005. Genomic homology of ORF 5 gene sequence between modified live
372 vaccine virus and porcine reproductive and respiratory syndrome virus challenge isolates
373 is not predictive of vaccine efficacy. *Journal of Swine Health and Production* 13:246-
374 253.
- 375 Park C, Choi K, Jeong J, and Chae C. 2015. Cross-protection of a new type 2 porcine
376 reproductive and respiratory syndrome virus (PRRSV) modified live vaccine (Fostera
377 PRRS) against heterologous type 1 PRRSV challenge in growing pigs. *Veterinary
378 Microbiology* 177:87-94. DOI: 10.1016/j.vetmic.2015.02.020
- 379 Park C, Seo HW, Han K, Kang I, and Chae C. 2014. Evaluation of the efficacy of a new
380 modified live porcine reproductive and respiratory syndrome virus (PRRSV) vaccine
381 (Fostera PRRS) against heterologous PRRSV challenge. *Veterinary Microbiology*
382 172:432-442. DOI: 10.1016/j.vetmic.2014.05.030
- 383 Savard C, Alvarez F, Provost C, Chorfi Y, D'Allaire S, Benoit-Biancamano MO, and Gagnon
384 CA. 2016. Efficacy of Fostera PRRS modified live virus vaccine against a Canadian
385 heterologous virulent field strain of porcine reproductive and respiratory syndrome virus.
386 *Canadian Journal of Veterinary Research* 80:1-11.
- 387 Shi M, Lam TT, Hon CC, Murtaugh MP, Davies PR, Hui RK, Li J, Wong LT, Yip CW, Jiang
388 JW, and Leung FC. 2010. Phylogeny-based evolutionary, demographical, and
389 geographical dissection of North American type 2 porcine reproductive and respiratory
390 syndrome viruses. *Journal of Virology* 84:8700-8711. DOI: 10.1128/JVI.02551-09

- 391 Stoian AMM, and Rowland RRR. 2019. Challenges for porcine reproductive and respiratory
392 syndrome (PRRS) vaccine design: reviewing virus glycoprotein interactions with CD163
393 and targets of virus neutralization. *Veterinary Sciences* 6:9. 10.3390/vetsci6010009
- 394 Yoon IJ, Joo HS, Goyal SM, and Molitor TW. 1994. A modified serum neutralization test for the
395 detection of antibody to porcine reproductive and respiratory syndrome virus in swine
396 sera. *Journal of Veterinary Diagnostic Investigation* 6:289-292.
397

Figure 1

Records of daily body temperature and fever of the mock, UnV and MLV groups after challenge with PRRSV.

(A) The body temperatures were measured daily from -5 to 20 DPC. (B) The days in which body temperatures were greater than 40°C were calculated for pyrexia quantification. Each dot represents an experimental individual and the lines indicate the mean value of each group. Statistically significant differences are revealed with asterisks (*, *** for $P < 0.05$ and 0.001, respectively).

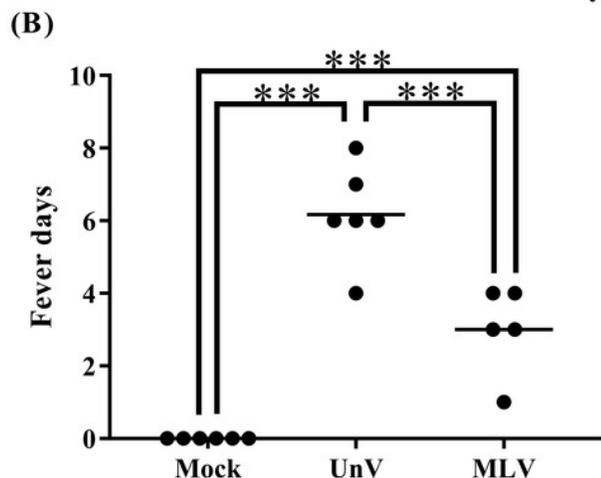
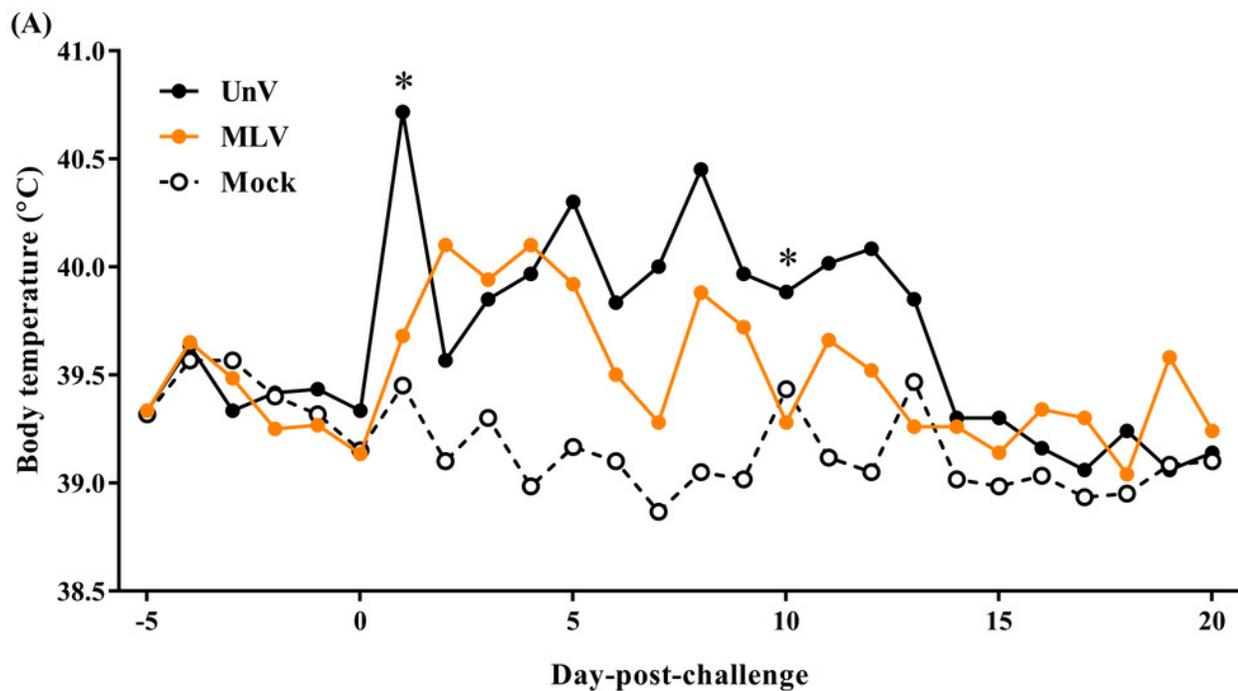


Figure 2

Records of clinical signs of the mock, UnV and MLV groups after PRRSV challenge.

(A) Clinical signs of activity and (B) respiratory distress were measured on a daily basis after challenge.

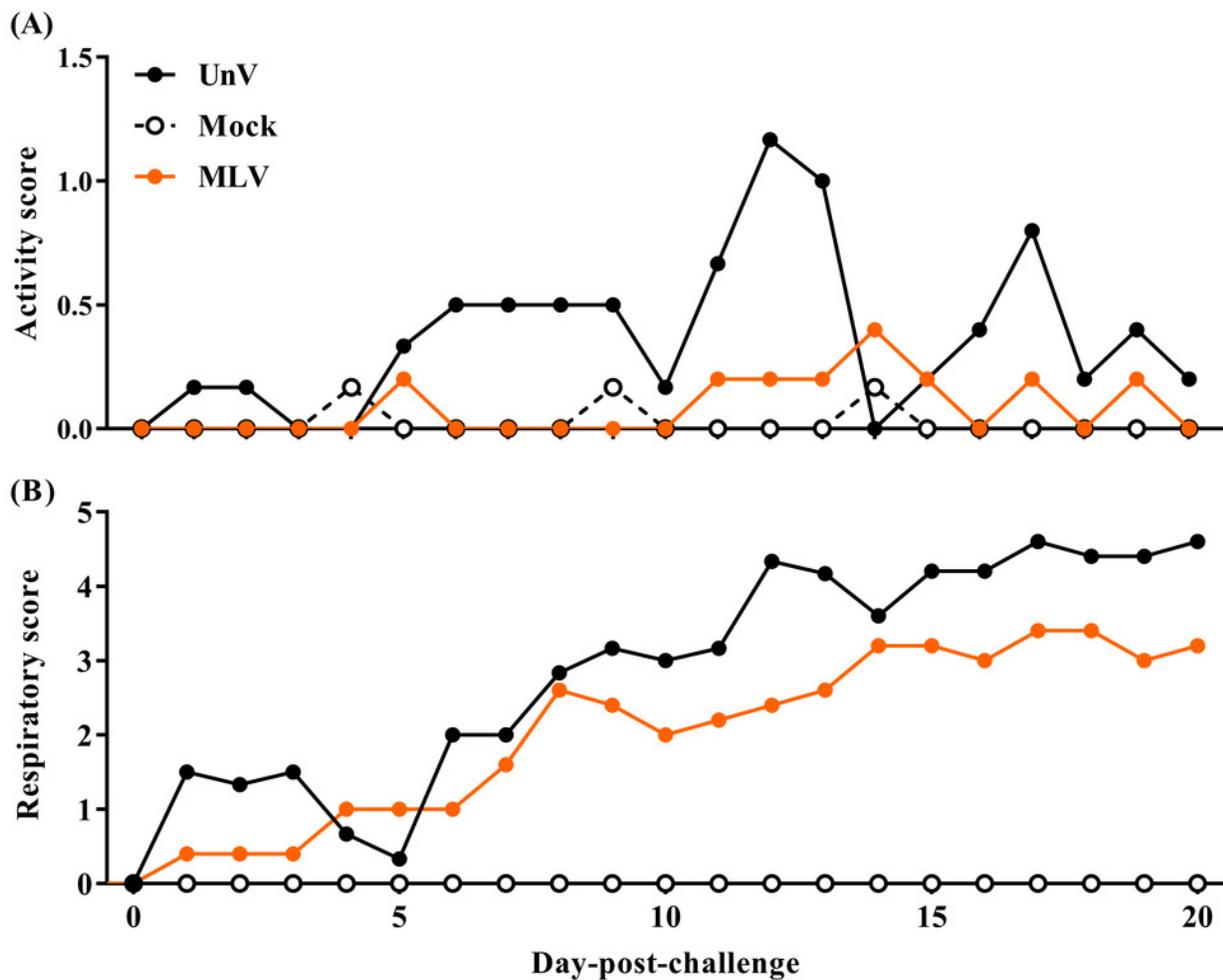


Figure 3

Records of growth performances of the mock, UnV and MLV groups after PRRSV challenge.

All pigs were weighed at 0, 10 and 20 DPC for calculating the average daily weight gains (ADWG) in the acute (0-10 DPC) and whole phase (0-20 DPC) of infection. The values are indicated as mean \pm SEM and the number of asterisks represented the levels of statistical significance (* for $P<0.05$ and *** for $P<0.001$). Average daily food intake (FI; kg food/pig) and the food conversion rate (FCR; food intake/body weight gain) were also calculated.

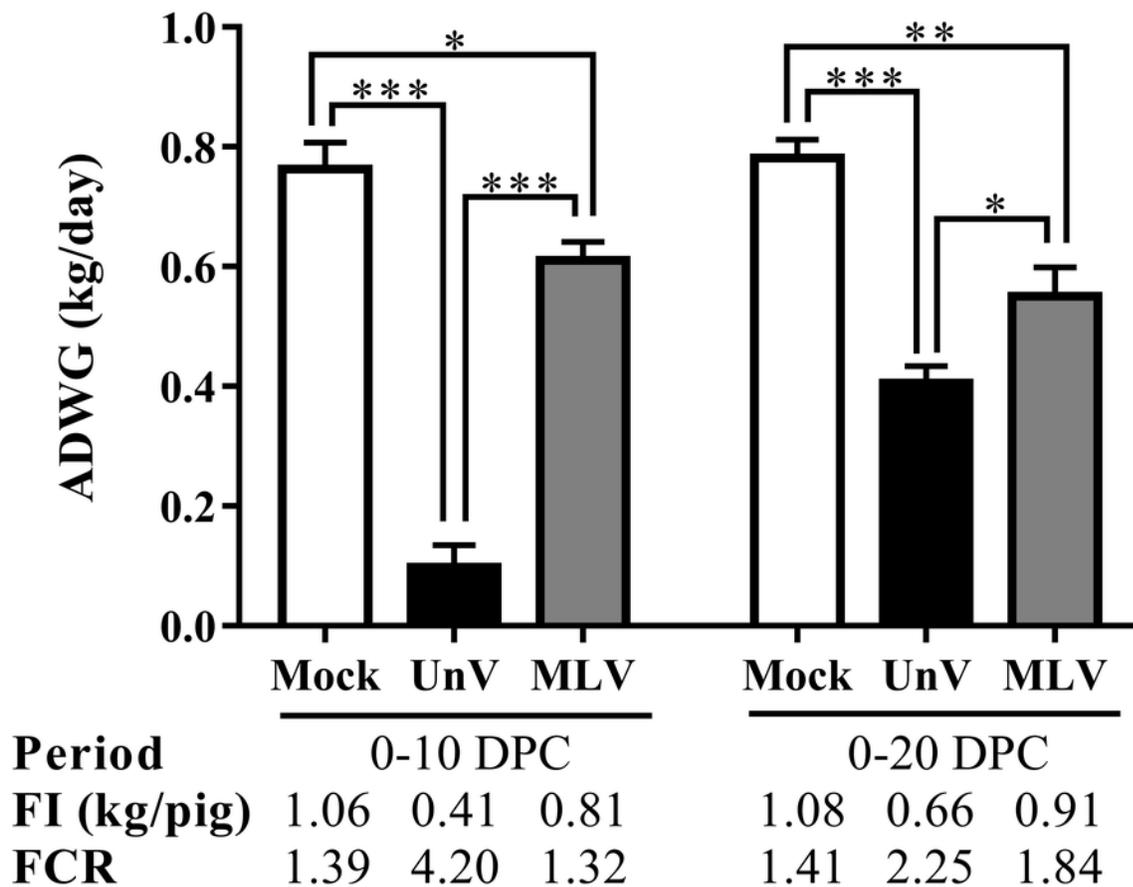


Figure 4

Results of macro- and microscopic interstitial pneumonia of the mock, UnV and MLV groups after PRRSV challenge.

Both (A) macro- and (B) microscopic interstitial pneumonia (IP) lesions were scored. All data was indicated as mean \pm SEM and the number of asterisks represented the levels of statistical significance (** for *P* value less than 0.01).

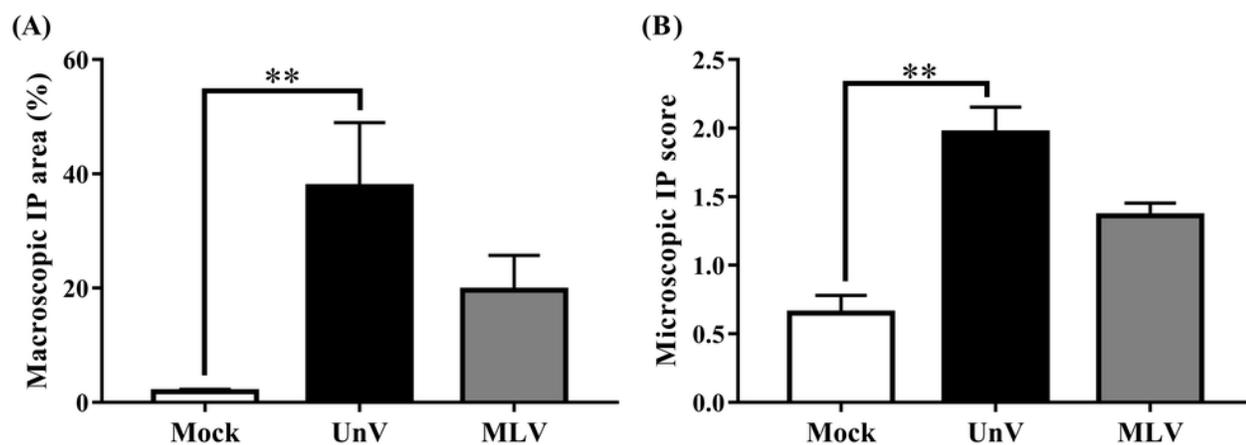


Figure 5

Changes of PRRSV viremia titers of the UnV and MLV groups after vaccination with MLV and challenge with PRRS field isolate.

The serum samples were submitted for PRRSV viremia quantification by using real-time RT-PCR. Each dot represents an experiment individual and the lines and error bars indicate mean \pm SEM of each group. Statistical significances ($P<0.05$) between the UnV and MLV groups are indicated by asterisks (*).

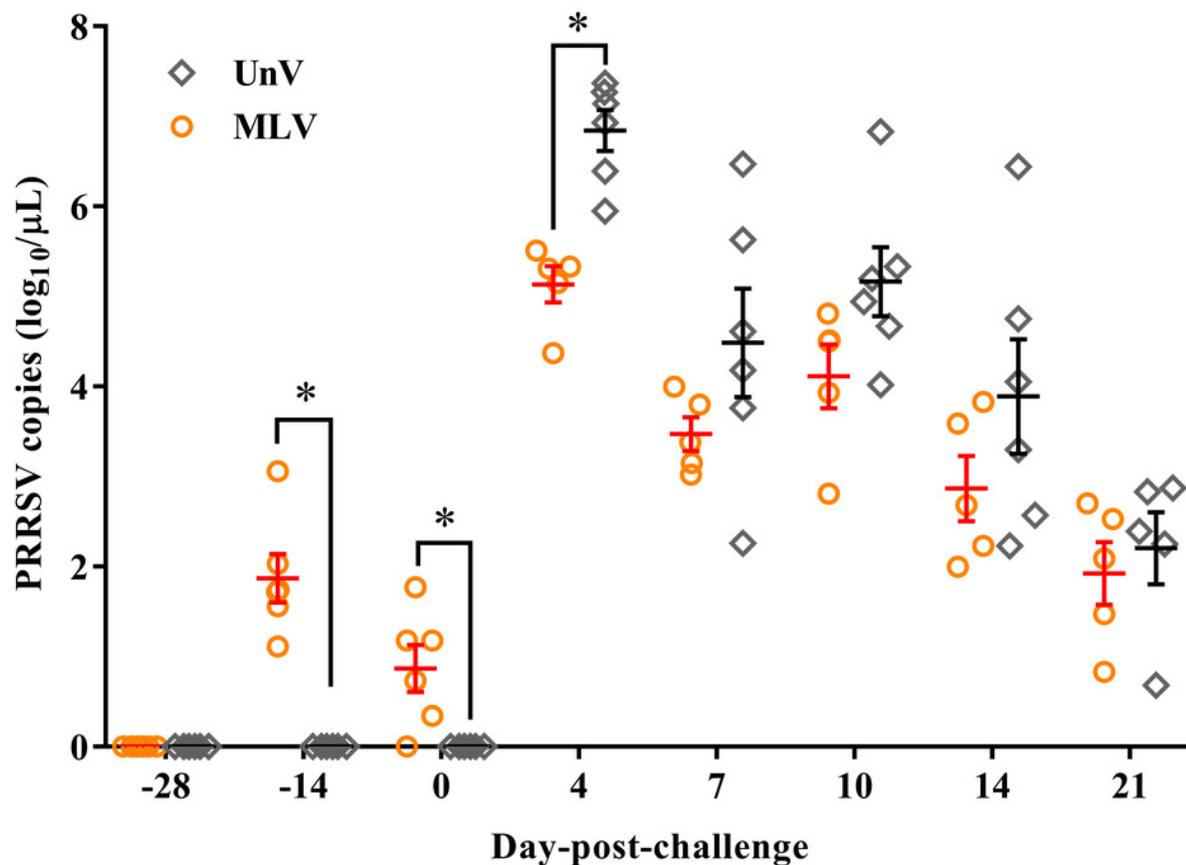


Figure 6

Quantifications of PRRSV-specific antibody and PRRSV-stimulated IFN- γ secreting cells of the mock, UnV and MLV groups.

(A) The measurement of serum PRRSV-specific antibody was performed using commercial ELISA kits. (B) Purified PBMCs were stimulated with the challenge PRRSV, TSYM-isolate, for recalling IFN γ responses. All data was presented as mean \pm SEM and asterisk (*) for statistically significant differences between the UnV and MLV groups ($P < 0.05$).

